

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

```
Run on: September 7, 2002, 19:53:06
; Search time 3270.98 Seconds
; (without alignments)
11291.826 Million cell updates/sec
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Title:      US-09-993-874-1
Perfect score: 1765
Sequence:   1 tcagtcagactttagga.....aaaaaaaaaaaaaaaaaa 1765

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database :
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5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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26: em_ro:*
27: em_sts:*
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29: em_vl:*
30: em_hcg_h
31: em_htg_l
32: em_htg_o
33: em_htg_o
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	Score	Match	Length	DB	ID	Description

1	1763.4	99.9	1765	3	AFI39644	AFI39644 Phrixothr
2	1284.4	72.8	1760	3	AFI39645	AFI39645 Phrixothr
3	582	33.0	1659	6	I40164	I40164 Sequence 1
4	581.6	33.0	1647	5	AF32853	AF32853 Pyrococell
5	581.6	32.9	1659	6	AF32853	I40165 Sequence 2
6	580.4	32.9	1922	3	L39928	L39928 Pyrococella
7	580.4	32.9	1922	3	PIDLUICR	X89479 L.noctiluca
8	577	32.7	1831	3	PU31240	U31240 Photuris pe
9	575.2	32.6	2193	6	AX074306	AX074306 Sequence
C	575.2	32.6	2193	6	AX074308	AX074308 Sequence
C	575.2	32.6	2268	6	AX074303	AX074303 Sequence
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17	565.2	32.0	1639	6	AX098283	AX098283 Sequence
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25	556	31.5	1639	6	AX098291	AX098291 Sequence
26	555.6	31.5	1639	6	AX098324	AX098324 Sequence
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32	552.8	31.3	1811	6	A37556	A37556 Sequence 22
33	552.8	31.3	4672	12	CVE277960	CVE277960 Cloning v
34	552.8	31.3	4674	12	XX002437	U02437 Cloning vec
35	552.8	31.3	5067	12	AF093685	AF093685 Luciferas
36	552.8	31.3	5499	12	AF093684	AF093684 Luciferas
37	552.8	31.3	5596	12	CYLUCLIC	U25266 ligation-in
38	552.8	31.3	5597	12	CVPGL2BAS	X65323 Cloning vec
39	552.8	31.3	5675	12	AF053698	AF053698 Reporter
40	552.8	31.3	5688	12	AF053461	AF053461 Reporter
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42	552.8	31.3	5714	12	AF167311	AF167311 Reporter
43	552.8	31.3	5743	12	AF053462	AF053462 Reporter
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45	552.8	31.3	5789	12	CVPGL2PPO	X65326 Cloning vec

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1	2	3	4	5	6	7	8	9	10	11	1																																																																																								

Qy 1741 aaaaaaaaaaaaaaaaaa 1765
Db 1741 AAAAAAAAAAAAAAAAAA 1765

RESULT 2
AF139645 1760 bp mRNA linear INV 14-DEC-1999
LOCUS Phrixothrix hlirtus red-bioluminescence eliciting luciferase mRNA,
DEFINITION complete cds.
ACCESSION AF139645
VERSION AF139645.1 GI:4959886
KEYWORDS Phrixothrix hlirtus.
SOURCE Phrixothrix hlirtus.
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Elateriformia; Cantharoidae; Phengodidae; Phrixothrix.
REFERENCE 1 (bases 1 to 1760)
AUTHORS Vliani,V.R., Bechara,E.J. and Ohmiya,Y.
TITLE Cloning, sequence analysis, and expression of active Phrixothrix
rillroad-worms luciferases: relationship between bioluminescence
spectra and primary structures
JOURNAL Biochemistry 38 (26), 8271-8279 (1999)
MEDLINE 9315203
PUBMED 10387072
REFERENCE 2 (bases 1 to 1760)
AUTHORS Vliani,V.R. and Ohmiya,Y.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-1999) Biochemistry, Shizuoka University, 836,
Oya, Shizuoka 422, Japan
FEATURES
source location/Qualifiers
1..1760
/organism="Phrixothrix hlirtus"
/db_xref="taxon:94779"
41..1681
/note="PhRE"
/codon_start=1
/product="red-bioluminescence eliciting luciferase"
/protein_id="AAD34543.1"
/db_xref="GI:4959887"

CDS
/translation="MEERNVYNGRPDRDLPFGNAGLQYLSLYKSYITTDIAHT
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NDMYTEREMIGHILSKPCLMFCSKSLPFLIKYOKHIDFLKRYVIDSMVDINGEC
VFSEDSNTHADFPVFNPKFEPLEFETALIMTSGTGPKGVISHRSITTRFV
SSDPIYGRFARPOPSILAIAPFHAFGLFLAYFPVGLKIVMKKEGGEFLTION
YKIASIVPPRIMVYLAKEPLVDENCSLSLEIASGSGSLERDADKAKRLKYHGIL
OGYGLTETCSALILSPNDRELKKAIGTPMRYVYKVIDITGTGALGPREGEICFKS
OMLMKGYHNHNPQARDALDKDGMHTGDLGYDDRFYVVDRLKELIKRYGVOVAPA
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BASE COUNT 598 a 311 c 342 g 509 t
ORIGIN

Query Match 72.8%; Score 1284.4; DB 3; Length 1760;
Best Local Similarity 84.9%; Pred. No. 9.9e-256;
Matches 1473; Conservative 0; Mismatches 256; Indels 5; Gaps 3;

Qy 13 tttagggatcaaaatggaagaagaacattagcgatggagagcgtcctcgatgataagt 72
Db 28 TTTTGAGATCAAAATGGAAGAAAGAAACGTTGTGAATGAGATCCTCCGATCTACT 87
73 caatcctgcgcggaagaacaacattacccaatcatgtataaattgcatctttcc 132
Qy 88 TTTTCTGCGACAGACAGACATCAATTTATATCAATCATTTATTAATTTCTATATTAC 147
Db 133 tgaagcaataatcgatgctcatcaaatgaaagtaataatcatatgctcgaataatctgaaac 192
Db 148 TGACGGAATTAATTCGATGCCCATACCAATGAAGTATATCATATGCTCAAAATTTTGAAC 207
Qy 153 cagcgcgcgcttagctgttagatagaacaataatgcttgaaatgaaacaatgctgtgag 252
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Db 208 CAGCTGCCGCTTGCGCATGTTAGTCTAGAAAAATATGCGTTGATCATACATGTTGTGCG 267
Qy 253 tgatgcaatgaaacaataataaacttttaactgcctgcctgcttactactaag 312
Db 268 AATATGCACTGAAACAAACATACACTTTTGTGGCCCTTTAATTTGCGCTTTATACCAAG 327
Qy 313 aatbaccagtagcaacaataatgataatgatacagaatggaagatgtaactgtaactgaa 372
Db 328 AATACCAATGCGCAACATCAATGATGTACACAGAAAGGAGATGATGGCATTTGGAA 387
Qy 373 tatatcaaaccaacatcatatgtttagttcagaagaagcaccocgcttatcttgagat 432
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Db 508 TGGCGTTGAATGCGATTTTATGCTTTGATTCACGTAATACGATCATGATGATCAGT 567
Qy 553 gtcatttaacccaagaagaatcttgatcccttgaaaaaatcgcatatataatgtaacatc 612
Db 568 GAAATTTAACCCAAAAGAGATTGATCCCTTGGAAGAACCGGATTAATATGACATCATC 627
Qy 613 tgaagaacttgatgacctgaagggtgtagtactgaagccaagaagtcataactaagaatc 672
Db 628 TGGAACCACTGGATTCCTTAAGGGGTATTAATAGCCATAGAGATATACATTAAGATT 687
Qy 673 cgtcaatgaaggaatcccatltaatgacatcgtaacgttaccacaacaataatcttcc 732
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Qy 853 ttacaataatcccaatctatgtagtggccctccagttatgtagtcttggctaaagcc 912
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Qy 913 attagtcgtcaaatcgaattatcgaagcttaacgaagttgctacccgagggagctcttc 972
Db 928 ATTAGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 987
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Qy 1150 tgggaagcgcctgaagcaggaaggaaggaaggaatatacttccaaagtgaaatgatac 1209
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Qy 1210 gaaagataatcaacaatcgcgaagcaactatgatactatgacaagaatgctgtgct 1269
Db 1228 GAAAGATATCAACAACATCCCAAGCAACTGCTGATGCTTTGACAAAGATGTTGAGCT 1287
Qy 1270 tcatctggaatgattggaatgataagcagaagaatgaaattccttatatgattgataag 1329
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DB 1587 TTTATAGTACTATTTCCAAAAGGCCCAACAGAAACTCATGAGAAACGAACTCCGAGCA 1646
QY 1629 taltgcccagcgagcaacaataataataagtaagtaagtaagtaagtaagtaag 1688
DB 1647 TATTTGCCCGGAAACAGGCAAAATCAAAATTAACCTCATATATGCTTTGTTATTA 1706
QY 1689 aatgatatataaagaattttagaacttaataacttaacttaacttaacttaactaa 1742
DB 1707 AATGTATGTAATCAAAATTTAGAACCTAATACATTCATTGAGAGCTTAATAA 1760

RESULT 3
LOCUS 140164 1659 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5618722.
ACCESSION 140164
VERSION 140164.1 GI:2083169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1659)
AUTHORS Zemo, S., Shiraishi, S., Inouye, S. and Salgo, K.
TITLE Photuris firefly luciferase gene
JOURNAL Patent: US 5618722-A 1 08-APR-1997;
FEATURES
Source Location/Qualifiers
1..1659
BASE COUNT 321 a 193 c 268 g 265 t 612 others
ORIGIN

Query Match 33.0%, Score 582; DB 6; Length 1659;
Best Local Similarity 43.6%; Pred. No. 2e-110;
Matches 704; Conservative 247; Mismatches 655; Indels 9; Gaps 2;

DB 249 RAATGVTGNCARTTYYTATGCCNATHITGCGNCNTNTATGNGNCTMCNACNCC 308
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DB 309 NCCNMAAAYGAYATHTAAAYGABMGNGARNTNTAAAYTCNTYTNCNATHITCNARCC 368
QY 385 aactcatgattagttcaagaagaagcactccgcttactctgagatgacagaactc 444
DB 369 MNCNGTNGTNTTACCTCMGNBAITCNTNCAARAARATHTYNGGNTNCATPCNMGNNT 428
QY 445 aagttcataaaaaaagctgtagtatacgaatagatagatagatagatagatagatag 504
DB 429 NCCNATHATHAARAARATHTATHTNCAVGNANARAARGAYTAYTNGGNTATCATRC 488
QY 505 cgtatcactctgtgtgacgcttatactgacacacacttgcattgcatttacaac 564
DB 489 NATGARTNTTAYTGAAGARCAVGTNCCNCAAYTAYTAYGNTGCTNTTYAARCC 548
QY 565 aaaaagatttgatccctcgaaaaaatcgcatlaatttgcatcatctggaacactgg 624
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QY 625 attgcctaagggtgtagtactgagccatagaagtaactaagaattcgttcatagcag 684
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DB 1326 RTAAYAAAGNTATCARGTNCCNCGNCAARYTNGARGCNYTNTYNTNCAVCAACNTT 1385

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Db	1446	NGTNGTNGTNTNARGARGAGNAARTCNATHCNCNARAARGARATHCAAGATTAATGCTNCC	1505
QY	1525	agcaagaatcaccacaaagaacatctcgaagcggtgtcgtcatgttgaagacagatattcc	1584
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QY	1585	gaagagccctactggaagaactcaagaagaagcgtcgcgaagaataattgcccag	1639
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LOCUS	AF328553	1647 bp	mRNA	linear	INV	17-DEC-2001
DEFINITION	Pyrococella rufo luciferase mRNA, complete cds.					
ACCESSION	AF328553					
VERSION	AF328553.1	GI:12018177				
KEYWORDS						
SOURCE	Pyrococella rufo.					
ORGANISM	Pyrococella rufo Eubacteria; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia; Cantharoidae; Lampyridae; Pyrococella. Lee, K.S., Park, H.J., Bae, J.S., Go, T.W., Kim, I., Sohn, H.D. and Jin, B.R. Molecular cloning and expression of a cDNA encoding the luciferase from the firefly, Pyrococella rufo J. Biotechnol. 92 (1), 9-19 (2001)					
TITLE						
JOURNAL						
MEDLINE	21490298					
PUBMED	11604168					
REFERENCE	2 (bases 1 to 1647)					
AUTHORS	Lee, K.S., Park, H.J., Bae, J.S., Lee, K.S., Shon, H.D. and Jin, B.R. Direct Submission Submitted (12-DEC-2000) Laboratory of Genetic Engineering of Natural Products, College of Natural Resources and Life Science, Dong-A University, 840 Hadan 2 dong, Sahaqu, Pusan 604-714, Korea					
TITLE						
JOURNAL						
FEATURES						
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CDS						
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ORIGIN						

Query Match	33.0%	Score 581.6	DB 3	Length 1647
Best Local Similarity	60.6%	Pred. No. 2.4e-110		
Matches 991	Conservative 0	Mismatches 634	Indels 9	Gaps 2

QY	36	aaaaacattaggaatggaagcgcttcctctgtaataatgcatcctcgtgctcgagagacaac	95
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Qy	96	aattaacaaatcatgtatataaattlgaacatttcccttccgaagaaat-----aalcagtg	149
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Qy	150	ctcalacaaatgaaglaatalcalatcagtcacaaatltgaaacagctgcgcgtactgctg	209
Db	137	CACACGCGAGAGGTAAATATTTACATATTTCCGAAATTTTGAATGCTCTCCGATATGGCG	196
Qy	210	ttagatagaacaaatagtcgttgaatgaacaacatgtltyggltgatcagtgaaaca	269
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Qy	270	ataaaactttttaaaccgctccctgctgcttcttactacttaggaataaccagtagcaaat	329
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Qy	390	tcaatgttagtccaagaagaagacatcccgcttatcttgagagtagacgcaaatcctaatt	449
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Qy	450	tcaatlaaaaagctgtagtlaacgaatgaacagatlaaagcaatlaagcgttgaatgcgat	509
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Qy	510	ctacccttgttcgacgctataactcagcacacacttgatccatgtlcatcattacaccaaaag	569
Db	497	ACTGCTCATTTGAATACATCTACCTCAGAGTTTAAATGAATATGATTTACATACCGGATTT	556
Qy	570	atttgcatacccttcgaaaaaatcgcattaatatctgcaatcactcgtgaacaaacttgatgc	629
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Qy	630	ctaaagcgttagtactcagacacataagaagcttaactaataaagctcgtcagcaagagatc	689
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Qy	690	ccattatcagcactcgcagcttcccaaaaacatcaatctcttccactagtagccgtlccatc	749
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Db	737	ATGGTTTTGGAAATGTTTAAACAATTAAGATATTTTAAACGTTGTGATTTCCGTATTTGGCTTA	796
Qy	810	tgaagaaaatttgagagcgccacttctcttaaaaacatacagaattacaatatccccacta	869
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Qy	870	ttgtagtgcgccccccagatlaagtglttcttggtcctlaaaagcccatagtcgaatcaatcg	929
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Db	917	ATTATTCACAACTTACATGAATTTCTTCCGTTGGAGCTCCTCTCGGAAAGAAATTTGGAG	976
Qy	990	aagcagtagcgaagaagttgaatattacactcggaaatcaacaagatataatgaataactgaa	1049
Db	977	AAGCGGTGACAAAACGTTTTTAAGTTTGGCGGGCATACACAGAGGGACGGACTTTACCGAAA	1036
Qy	1050	cttgcgtgcgtgaatgataaccctcataatcgtctgaaaaacaggttcaacttggaaagc	1109
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Db 1206 YAAYCCNGARGCNCACGCCGARYTNATHGAYARGARGCNTGANTHCAYTCNGNGCAVAT 1265
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Oy 1345 atacaagagatacaggtgtgctgtgactgtgaaatctgtcttacaacatccaag 1404
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Db 1506 NGNCARGTNCNTCMTNAARAARYTNMNGCNGNGTNGARTTYGTMAARGARGTNC 1565
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RESULT 6
LOCUS PIRLUCTF 1922 bp mRNA linear INV 05-DEC-1995
DEFINITION Pyrococella miyako (clone PB-PmL41) luciferase mRNA, complete cds.
ACCESSION L39928
VERSION L39928.1 GI:695386
KEYWORDS luciferase.
SOURCE Pyrococella miyako (clone PB-PmL41) whole body cDNA to mRNA.
ORGANISM Pyrococella miyako (clone PB-PmL41) whole body cDNA to mRNA.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Elateriforma; Cantharoidea; Lampyridae; Pyrococella.
REFERENCE 1 (bases 1 to 1922)
AUTHORS Ohmura, Y., Ohba, N., Toh, H. and Tsuji, F.
TITLE Cloning, expression and sequence analysis of cDNA for the
luciferases from the Japanese fireflies, *Pyrococella miyako* and
Hotaria parvula
JOURNAL Photochem. Photobiol. 62 (2), 309-313 (1995)
MEDLINE 96061635
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BASE COUNT 607 a 330 c 398 g 587 t
ORIGIN

Query Match 32.9%; Score 580.6; DB 3; Length 1922;
Best Local Similarity 59.9%; Pred. No. 3.8e-110;

Matches 1011; Conservative 0; Mismatches 669; Indels 9; Gaps 2;
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Oy 76 tccgtgtcgagcagaacaacatataccaatcatgtataaattgtgacttcttcga 135
Db 62 GGATGGAAGTCCCGGAGAACAAATTCACAAAGCGATGAAGAGATGACAGAGTTCAGG 121
Oy 136 agcaata-----atgatgctcatcaaatatgaagtaatatataatgacccaatttga 189
Db 122 GACAAATGCTTTTACATGATGCACCGCAGAGTAATATTAACATATTCGAAATATTTGA 181
Oy 190 aaccagctgcgcgttcgtgctgtatagaacataatgcttgaagaagaacatgtc 249
Db 182 AATGCTTTGCCATTTAGCCGAAACTATGAAGAGATACGGACTTGGTTTACAAACCCACAT 241
Oy 250 ggggtatgcaatgaaacaataataacttlttaactcgttcctgtcgttataact 309
Db 242 TCGTGTGTAGGAAGAACTTCTCTCAGTTTATGCTGTATGCGGTGACACTATTTAT 301
Oy 310 aggaataacagtagcaacaatcaatataatgtacacagaatggaagtttaactgtcatt 369
Db 302 TGGGGTTGGAGTTGCACCAACAATGATATTTTACAATGAACGTAATTTACACAGTTT 361
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Db 842 ACATTTATAAATTCAAAGTGGCTGTGCTGATCCCTCATTTTTCCTTCCCAAG 901
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RESULT 9
AX074306 2193 bp DNA linear PAT 06-FEB-2001
LOCUS Sequence 20 from Patent WO0104310.
DEFINITION AX074306
ACCESSION AX074306
VERSION AX074306.1 GI:12710492
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
1 (bases 1 to 2193)
REFERENCE
AUTHORS
Weber, E.R., Wood, K.V. and Hall, M.P.
Fc epsilon receptor-luminescence inducing protein chimeric nucleic acid molecules, fusion proteins and uses thereof
Patent: WO 0104310-A 20 18-JAN-2001.
Heska Corporation (US) ; PROMEGA CORPORATION (US)
location/Qualifiers
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BASE COUNT 716 a 461 g 648 t
ORIGIN

Query Match 32.6%; Score 575.2; DB 6; Length 2193;
Best local Similarity 60.0%; Pred. No. 4, 9e-109;
Matches 980; Conservative 0; Mismatches 648; Indels 6; Gaps 1;
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DEFINITION Sequence 22 from Patent WO0104310.
ACCESSION AX074308
VERSION AX074308.1 GI:12710494
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SOURCE
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synthetic construct.
artificial sequence.
REFERENCE
1 (bases 1 to 2193)
AUTHORS
Weber, E.R., Wood, K.V., and Hall, M.P.
TITLES
Fc epsilon receptor-1 luminescence inducing protein chimeric nucleic
acid molecules, fusion proteins and uses thereof
JOURNAL
Patent: WO 0104310-A 22 18-JAN-2001;
Heska Corporation (US) ; PROMEGA CORPORATION (US)
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LOCUS AX074303
DEFINITION Sequence 17 from Patent WO0104310.
ACCESSION AX074303
VERSION AX074303.1 GI:12710489
KEYWORDS
SOURCE
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artificial construct.
artificial sequence.
1 (bases 1 to 2268)
AUTHORS Weber E.R., Wood K.V. and Hall M.P.
TITLE FC epsilon receptor-immunescence inducing protein chimeric nucleic acid molecules, fusion proteins and uses thereof
JOURNAL Patent: WO 0104310-A 17 18 JAN-2001.
Heska Corporation (US) ; PROMEGA CORPORATION (US)
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 VERSION AX074305.1 GI:12710491
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 artificial sequence.
 1 (bases 1 to 2268)
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 1 Weber,E.R., Wood,K.V. and Hall,M.P.
 Fc epsilon receptor-luminescence inducing protein chimeric nucleic
 acid molecules, fusion proteins and uses thereof
 Patent: WO 0104310-A 19 18-JAN-2001;
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 Heskia Corporation (US) ; PROMEGA CORPORATION (US)
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QY	1517	tttatctgaagcaacaagctcactccaacaaagaactctcgagcgcgtgtgaltglaag	1576
Db	138	TTTGTGTTCCAGTCAAGTGTTCACACACCAAAATGGCTACGTCGTGGGGTGAAATTTTGGAT	79
QY	1577	agttctcgaagaagccctacttgcgaanaactcatcagaagaagagctcgcgaatatctgc	1636
Db	78	GAAATTTCCCAANAGCTACACTGGAATAATTGCACGAAAGAGTTTAAAGACAAATGTTGAA	19
QY	1637	cagcgcagcaccaca 1650	
Db	18	AAACACAATCTAA 5	
RESULT	13		
LOCUS	AX074300	1638 bp	DNA
DEFINITION	Sequence 14 from Patent WO0104310.		
ACCESSION	AX074300		
VERSION	AX074300.1	GI:12710486	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
CDS			

acid molecules, fusion proteins and uses thereof
Patent: WO 0104310-A 16 JAN-2001;

Hebeka Corporation (US) ; PROMEGA CORPORATION (US)

Location/Qualifiers

1. 1638
/organism="Photuris pennsylvanica"

/db_xref="taxon:41716"

BASE COUNT 506 a 319 c 254 g 559 t

ORIGIN

Query Match

Best Local Similarity 32.5%; Score 573.8; DB 6; Length 1638;
Matches 978; Conservative 0; Mismatches 647; Indels 6; Gaps 1;

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QY 26 atggaagaagaacattagcgatggagagcgtccctgataatagccatcgtgctg 85
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QY 86 gcaagacaacatataccaatcatgtatataattgcatcttctctgaa-----gca 139
Db 1578 GCTGAGACAGATGTTTACGCAATTCCTCGGTATCCAGATATTTACGATGCAATTCGA 1519
QY 140 ataatgcatcctatacaaatgaaatatacattgctcaaatattgaaacagctgc 199
Db 1518 TTGACAAATGCTCATACAAAGAAATGTTTATATGAAAGATTTTAAATTTGTCGTG 1459
QY 200 cgtctatcgttagatagacaatatagcttgaatgaagaacatgtgtgggtgtatgc 259
Db 1458 CGTTTACGGGAAGTTTAAAGATGATGATTAACAAACACACCAATTAAGCGGTGTG 1399
QY 260 agtgaagaacataaacttttaactcctgctcgtgctgcttataactagaatacca 319
Db 1398 AGTGAATAATGTTTGCATTTTCTTCTTATATGCAATTCATTTGATCTTGAATTAAT 1339
QY 320 gtgacaacatcaatataatgatacagatagagagtttaactgcatlagaatataca 379
Db 1338 GCAGCACTTGTATGATTAATACATTTGAACGTAATTAACACAGTCTTGGTATTTGA 1279
QY 380 aaacaacatcatatgtttagtcaagaagacatcccgcttacttctgagatagagcaa 439
Db 1278 AAACCCAGCATATTTTGTTCACAGAAATCTTTCAAAAGTACTGATGTAATAATCT 1219
QY 440 aaactaagtcttaaaaaagtcgagtatatacagatagacatgtaagacaattagtcgt 499
Db 1218 AATTTAAATATGATAGAACTATTTATTTAGACTTAATGAAACAACTTAGAGAGGTAT 1159
QY 500 gaatgcatlactaccttctgtgacgttatactgaccacacacttgaatcatcgttcat 559
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Db 1098 AAACCAAAATTTCTTTATATGAGACAGATCAGTTGCGTGTATGTTTCTTCTGTATNA 1039
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QY 980 gatctgcagaagcagtagaagaagttgaaattacactgtaacatatacagaatagga 1039
Db 678 GAAATTTGGGAGATGATGTAAGAAAAACGTTTAAATTTTAACTTTGTAGCAGGATATGA 619
QY 1040 ttaactgaactcgtcgtgctgtgaatgattaccccatcctaagtctgtgaaacagttca 1099
Db 618 TTTAACAGAAACCACTTCGCTGTTTAAATTTATACACGGACACTGACGTCAACCGGATCA 559
QY 1100 actggaagacccttgcacatataagctlaaagttttagatacactaactggaagcg 1159
Db 558 ACTGTAAATATGATACCATTTACGCTGTAAAGTTGTGATGATCCTTCAACAGGAAATTT 499
QY 1160 ctgagaccggggaagaagcggaataatagcttcaaatgaaatgattatgaagatata 1219
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QY 1220 tacaacaatccgaagcaactatgatactatgacaagaatggttgcctatcctgga 1279
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QY 1280 gatattgaltatcagaagaatgaaattcttataatgattgcatcgtatgaaagactt 1339
Db 378 GATATTTGCTTATTAATGACAAATGATGCGCATTTTATATGTGACAGGCTGAAGTCATTA 319
QY 1340 attaaatacaagagatataagtttgcgtgctgacagtggaataatccttataacat 1399
Db 318 ATTAATATAAAGGTTTATAGTTGACCTGCTGAATTTGAGGAATCTCTTACAAAC 259
QY 1400 ccaaglatgtcgtagtcggtgttactgagttccggaacgaatttgytgaacatctact 1459
Db 258 CGTATATTTGTTGATGACCGCGCTTACTGTATACCGGATGAAGCCGGGAGCTTCCA 199
QY 1460 gctgcttgggtgtttagaatcttgcgaagcgtcgtatgaaaggaagttcaagatttc 1519
Db 198 GCTGACGAGTGTGTGATGACAGCTGGAATAATTTCAAGAAATGCTCAAAATTTT 139
QY 1520 attgacagaagctacatccacaagaacatcttgcaggcgtgtgtatgttagacgt 1579
Db 138 GTTTCAGTCAAGTTTCAACACCAAAATGCGTACGTGTTGGGTTAAATTTTGGATGAA 79
QY 1580 attcgaagaagccctactggaagaactcatcgaagaagcctccgagaataattgcccag 1639
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QY 1640 cgaagcaccaaa 1650
Db 18 CACAAATCTAA 8
RESULT 15
LOCUS AX098293 1642 bp DNA linear PAT 02-APR-2001
DEFINITION Sequence 12 from Patent WO0120002.
ACCESSION AX098293
VERSION AX098293.1 GI:13537597
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial construct
REFERENCE
1 (bases 1 to 1642)
AUTHORS
Wood, K.V., Hall, M.P. and Gruber, M.
THERMOSTABLE INULINASES FROM PHOTURIS PENNSYLVANICA AND PYROPHORUS
plagiophthalmus and methods of production
Patent: WO 0120002-A 12 22-MAR-2001;
PROMEGA CORPORATION (US)
FEATURES
Location/Qualifiers
1. 1642
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 15:03:41 ; Search time 30.72 Seconds
(without alignments)
3069.083 Million cell updates/sec

Title: US-09-993-874-2
Perfect score: 2812
Sequence: 1 MEEBNIRHGERPRDIYHPSG.....KLIRKLEIFAPQAPKSKL 545

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mhc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*
15: SP:rivirus:*
16: SP:bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2812	100.0	545	5	Q9U4U8
2	2099.5	74.7	546	5	Q9U4U7
3	1583.5	56.3	550	5	Q27755
4	1557.5	55.4	550	5	Q27758
5	1534	54.6	547	5	Q27688
6	1519	54.0	552	5	Q94696
7	1515	53.9	552	5	Q94697
8	1511.5	53.8	548	5	Q26076
9	1510.5	53.7	548	5	Q9GPF9
10	1485	52.8	548	5	Q25118
11	1483	52.7	548	5	Q26304
12	1457.5	51.8	548	5	Q27348
13	1454	51.7	545	5	Q27757
14	1453.5	51.7	548	5	Q27321
15	1030	36.6	544	5	Q9VCC6
16	864.5	30.7	542	10	Q42943

17	847.5	30.1	636	10	Q42879	Q42879 lithosperm
18	847	30.1	548	10	Q48868	Q48868 populus bal
19	834	29.7	545	10	Q9SMH8	Q9SMH8 solanum tub
20	828	29.4	562	10	Q9FGW4	Q9FGW4 arabidopsis
21	826.5	29.4	540	10	Q94G19	Q94G19 populus bal
22	824.5	29.3	544	10	Q9LJ50	Q9LJ50 rubus idaeu
23	823.5	29.3	557	10	Q48869	Q48869 populus bal
24	820.5	29.2	544	10	Q9M0X3	Q9M0X3 arabidopsis
25	817.5	29.1	536	10	Q941M4	Q941M4 populus tom
26	816.5	29.0	536	10	Q941M3	Q941M3 populus tre
27	815.5	29.0	535	10	Q81139	Q81139 populus tre
28	810	28.8	546	10	Q9C5H2	Q9C5H2 arabidopsis
29	802	28.5	585	10	Q42880	Q42880 lithosperm
30	800	28.4	542	10	Q9F0T7	Q9F0T7 capsicum an
31	795	28.3	570	10	Q9LUJ6	Q9LUJ6 arabidopsis
32	790.5	28.1	556	10	Q9M7S2	Q9M7S2 lolium pere
33	783	27.8	580	10	Q9LMW8	Q9LMW8 arabidopsis
34	780	27.7	544	5	Q19339	Q19339 caenorhabdi
35	777.5	27.6	570	10	Q81140	Q81140 populus tre
36	777	27.6	579	10	Q94G18	Q94G18 populus bal
37	777	27.6	1549	10	Q9LMV7	Q9LMV7 arabidopsis
38	776	27.6	522	2	Q9K3W1	Q9K3W1 streptomyce
39	768.5	27.3	557	10	Q9M7S1	Q9M7S1 lolium pere
40	767.5	27.3	543	10	Q9LJ49	Q9LJ49 rubus idaeu
41	752.5	26.8	566	10	Q49414	Q49414 arabidopsis
42	746.5	26.5	542	10	Q9LQ12	Q9LQ12 arabidopsis
43	732	26.0	597	5	Q9Y158	Q9Y158 drosophila
44	719.5	25.6	570	10	Q9M7S3	Q9M7S3 lolium pere
45	708.5	25.2	591	10	Q9LJ51	Q9LJ51 rubus idaeu

ALIGNMENTS

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AC Q9U4U8
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LUCIFERASE.
OS Phrixochrix vivianli.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Elateriformia; Cantharoidea; Phengodidae; Phrixochrix.
OX NCBI_TaxID=94780;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9315203; PubMed=10387072;
RA Vivianli V.R., Bechara E.J., Ohmura Y.;
RT Cloning, sequence analysis, and expression of active Phrixochrix
RT railroad-worms luciferases: relationship between bioluminescence
RT spectra and primary structures.;
RL Biochemistry 36:8271-8279(1999).
RL EMBL: AF139644; AAD34542.1; -.
DR HSSP: P08659; ILCI.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PROSITE: PS00455; AMP-BINDING; 1.
SQ SEQUENCE 545 AA; 59756 MW; 3C7971D40E4BC119 CRC64;

Query Match 100.0%; Score 2812; DB 5; Length 545;
Best local similarity 100.0%; Pred. No. 6.5e+209;
Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MEEBNIRHGERPRDIYHPSGGOOLYOSLYKKFASPEPAIDAHTEYISYQAIFETSCRL 60
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QY 181 KQEDPLEKIALIMSSSGTGLPKGVVLSHRSILIRFVHSRDPYGRVYQTSILSLVPF 240
DB 181 KQEDPLEKIALIMSSSGTGLPKGVVLSHRSILIRFVHSRDPYGRVYQTSILSLVPF 240
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DB 301 YDLSLITEVATGAPLGKQVAEVAARLKLPGIIOGYGLTEPCCAVITPHNKKVGSNG 360
QY 361 RPLPYIKAKVLDNATGKALGPGERGEICFQSEIMKGYNNPEATIDTIDKQWMLHSGDI 420
DB 361 RPLPYIKAKVLDNATGKALGPGERGEICFQSEIMKGYNNPEATIDTIDKQWMLHSGDI 420
QY 421 GYYDEDEGNFFIYDRLKELIKYGYVAPAELENLLQHPISADAGVTVGPDEFGQLPAA 480
DB 421 GYYDEDEGNFFIYDRLKELIKYGYVAPAELENLLQHPISADAGVTVGPDEFGQLPAA 480
QY 481 CVALESKLTLEKEVODFIAAQVTPTKHLRGVVFVDSIPKPGTGLIRKELREIFAORA 540
DB 481 CVALESKLTLEKEVODFIAAQVTPTKHLRGVVFVDSIPKPGTGLIRKELREIFAORA 540
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DB 541 PKSKL 545
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RESULT 2

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Q90407 PRELIMINARY; PRT; 546 AA.
AC Q90407;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE RED-BIOLUMINESCENCE ELICITTING LUCIFERASE.
OS Phrixothrix hirtus.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Elateriformia; Cantharoidea; Phengodidae; Phrixothrix.
OX NCBI_Taxid=94779;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99315203; PubMed=10387072;
RA Viviani V.R., Bechata E.J., Ohmiya Y.;
RT "Cloning, sequence analysis, and expression of active Phrixothrix
RT railroad-worms luciferases: relationship between bioluminescence
RT spectra and primary structures.";
RL Biochemistry 38:8271-8279(1999).
DR EMBL; AF139645; AAD34543.1; -
DR HSSP; P08659; ILCT.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 546 AA; 60952 MW; 9349ABC931CC9A50 CRC64;
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Best Local Similarity 71.1%; Pred. No. 7.8e-154;
Matches 391; Conservative 84; Mismatches 66; Indels 9; Gaps 3;

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DB 1 MEEENIRHGERPRDIIVHPSAGQOLYOSLYKFAPEPATTIDHTNEVISYAOIFETSCL 60
QY 61 AVSIEOYLGNENNNGVGCSENNINFFNPLYLAALYLIGIPVATSDMYTDGELTGHINISKP 120
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DB 61 AVSLEKYGIDHNNVVAICSENNIHFFGPLIAALYQIIPATSDMTTEREMIGHLINISKP 120
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DB 121 TIMESSKALPLILRYOQNLSPFIKKVVIDSMVDINGECVSTFVARYPDTHFDPLSFPP 180
QY 181 KQEDPLEKIALIMSSSGTGLPKGVVLSHRSILIRFVHSRDPYGRVYQTSILSLVPF 240
DB 181 KQEDPLEKIALIMSSSGTGLPKGVVLSHRSILIRFVHSRDPYGRVYQTSILSLVPF 240
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DB 241 HHAFGFTLTSYFVVGKLVKVMKKFEGALFLKTIQNYKIPTIYVAPVAVFLAKSPLVDQ 300
QY 301 YDLSLITEVATGAPLGKQVAEVAARLKLPGIIOGYGLTEPCCAVITPHN-AVKTGST 359
DB 301 YDLSLITEVATGAPLGKQVAEVAARLKLPGIIOGYGLTEPCCAVITPHN-AVKTGST 359
QY 360 GRPLPYIKAKVLDNATGKALGPGERGEICFQSEIMKGYNNPEATIDTIDKQWMLHSGD 419
DB 360 GRPLPYIKAKVLDNATGKALGPGERGEICFQSEIMKGYNNPEATIDTIDKQWMLHSGD 419
QY 420 GYYDEDEGNFFIYDRLKELIKYGYVAPAELENLLQHPISADAGVTVGPDEFGQLPAA 477
DB 420 GYYDEDEGNFFIYDRLKELIKYGYVAPAELENLLQHPISADAGVTVGPDEFGQLPAA 477
QY 478 --PACVYLESGKLTLEKEVODFIAAQVTPTKHLRGVVFVDSIPKPGTGLIRKELREIFA 535
DB 478 --PACVYLESGKLTLEKEVODFIAAQVTPTKHLRGVVFVDSIPKPGTGLIRKELREIFA 535
QY 536 FAORAPSKL 545
DB 536 FAORAPSKL 545
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RESULT 3

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Q27755 PRELIMINARY; PRT; 550 AA.
AC Q27755;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FIREFLY LUCIFERASE (EC 1.13.12.7).
OS Photinus pyralis (North American firefly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Elateriformia; Cantharoidea; Lampyridae; Photinus.
OX NCBI_Taxid=7054;
RN [1]
RP SEQUENCE FROM N.A.
RA Croizier G.;
RT "Construction and utilization of an Autographa californica nuclear
RT polyhedrosis virus vector with a unique cloning site: expression of
RT genes amplified by the polymerase chain reaction.";
RL Submitted (FEB-1995) to the EMBL/Genbank/DBJ databases.
DR EMBL; X84846; CA59281.1; -
DR HSSP; P08659; IBA3.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Oxidoreductase.
SQ SEQUENCE 550 AA; 60731 MW; 0A1C749D0C96ADD CRC64;
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Best Local Similarity 55.5%; Pred. No. 6.1e-114;
Matches 305; Conservative 102; Mismatches 139; Indels 5; Gaps 3;

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QY 1 MEE-ENIRHGERPRDIIVHPSAGQOLYOSLYKFAPEP--ATIDHTNEVISYAOIFETS 57
DB 1 MEDAKNIKKGPAFPYFPLEDGTAGBQLHAKMKRYALVPGTIAFTDAHIEVNTIYAYFEFS 60
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Oy		58	CRLAVSIQCVLNNVNVGQSEKNNINFPNDVALAALGLGVATSNMNYMDGELTGLNI	17
Dd		61	VRLDAMKRICLTNHNRIWVCSENSLOFEPMPVLGALIGVAAPANDIYERELNSMTI	120
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Dd		121	SQPIIVVFVFSKGIOLKLNTQVKKLLIIQKIIMOSKTYDGFGSQSYTFVTSHLPFGNEFD	180
Oy		178	FTRPDFPLEKIALIMSSSGTTGLPKGVLSHNSLTIRVHSRDPIYGRTPVQSTLSL	237
Dd		181	FVPESFDDKKTIALIMNSSGSTGLPKGVALLPHRTACVRFSHARDPIFGNOIIPDTALLSV	240
Oy		238	VPRHHAFEMFTLSYFYVGLKVWLKKRREGALTLYKTONKIKPIIVAPPVWFLAKSPL	297
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Oy		298	VDQYDLSLTREVATGAPLGKDVAEAVALRKLLPGIIIOGGTLETCCAVITPHNAVKTG	357
Dd		301	IDKYDLNLHEIASGGAAPLSKEVEGAVALRHPLRGINGOGTLETTSALLITPEGDDKP	360
Oy		358	STGRPLPIRAKKVLDNMGTKALGCGEGEGLCFQSEMIMKGYNNPEATTIDDKGHLHS	417
Dd		361	GVGKAVPFEFEAKVVDLTGTGLTNORGELCVRPMISMGSVNPPENATNALIDKDGHLHS	420
Oy		418	GDIGYDVDEGNFFIYDRLKELTIKKYGQVAPAELLENLLQPSITADAGVGVDPDEFQGL	477
Dd		421	GDIAWDEDEHFIFYDRKSLIKTKKGQVAPAELESILLQHPNFDFDAGVAGLPDDDADEL	480
Oy		478	PAACVLESGETLTEKEVODEIAAQVTPTKHLRGVVFPVSDIPKPGTKLRKELREIF-	536
Dd		481	PAAVVLEHGKTMTEKEIVDVASQVYTAKKLRGGVFEVDEVPGLTKLDARKIREILI	540
Oy		537	-AQRAPRSKL 545	
Dd		541	KAKKGKSKL 550	
RESULT		4		
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IC	Q27758	PRELIMINARY;	PRT:	550 AA.
AD	Q27758:			
DT	01-NOV-1996 (TREMBLrel_01, Created)			
DT	01-NOV-1996 (TREMBLrel_01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel_19, Last annotation update)			
DE	FIREFLY LUCIFERASE (EC 1.13.12.7).			
GN	LUC.			
OC	Photinus pyralis (North American firefly).			
CC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
CC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;			
OX	NCLTaxID=7054;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Croizier G.;			
RT	"Construction and utilization of an Autographa californica nuclear			
RT	polyhedrosis virus vector with a unique cloning site: expression of			
RT	genes amplified by the polymerase chain reaction.";			
RL	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.			
DR	HML; X84847; CAA59282.1; -.			
DR	HSSP; P08659; IBA3.			
DR	InterPro; IPRO00873; AMP-Bind.			
DR	Pfam; PF00501; AMP-binding; 1.			
RM	PROSITE; PS00455; AMP_BINDING; 1.			
SO	Oxidoreductase.			
SEQUENCE	550 AA; 60602 MW; D963B300D030F119 CRC64;			

Query Match	55.48;	Score 1557.5;	DB 5;	Length 550;
Best Local Similarity	54.7%;	Pred. No. 6.2e-112;		
Matches 301;	Conservative 104;	Mismatches 140;	Indels 5;	Gaps 3.

Db	1	MEKANKIKKGRAPPEYPLEDGEAGEQLHAKKAKKRALVPGTIAFTDAHIEVNIITVAAEYFEKS	60
Qy	58	CRLAVSTIEQGLENNANNVAVCSSENNINFEENPVIALYLGIPVATSDNMTYDGLTGLNI	117
Db	61	VRLEAMKRYGLNHNHIVVCSSENSLOFEMFVLGALFIGAVALPANDIVNERELISMNT	120
Qy	118	SKAPIPMSSKALFLILIRVOONLSFIKKVVIVDSMYDINGECVSTFVARTHTDPLS	177
Db	121	SQPIVVVAVYSKKGLOKILNVQKKLPIDOKIIMDSKTDYOGFOSYTTVTSHLRPFGEHYD	180
Qy	178	FTPKDPPLLEKIALIMSSGCTGLPKGVLSHRSILIRFVSHBDPIYGTPTVQTSILSL	237
Db	181	FVPSFSDKRTIALIMSSGSGTSPKGVALPHRTACVRFSHARDPIGNOIIPDTALISV	240
Qy	238	VRFHNAAGMFTLSYFVVGGLKVYMLKKFEGALRLKTIQONKKIPIYVAPRVYMLKSL	297
Db	241	VRFHNGCMFTLGYLLICGFVRVYMLRPFEEELFLRSIQDKIDQSALCLVPLRFSFPAKSTL	300
Qy	298	VDQVDSLSTIEVANGAPRLGKDVAAEVAARLYKLGIIQGLTETCCAVMITPHNAVKTG	357
Db	301	IDKDLDSLHRIASGAPRLSKEVEANAKRHLRPIQNGVGLTETTSALILTPREGDDKPG	360
Qy	358	STGRPLRYIAKVLIDNATGKALGPERGECISFOSEMIKGYNNPEATIDTIDKOGYHLS	417
Db	361	AVGVGAVPFEKCKVVDLTGKTGLGNQSGELCVRQPMISGVYNDPEETNALLIDKDGHLHS	420
Qy	418	GDICGVDDGGEFFIVDRILKELIKKGVAPAELENNLLHPSIADAGVGVNDEFEGOL	477
Db	421	GDIAVWDEDEHFFIVDRILKSLIKKGVAPAELESSLLOHPNIFDAGVAGLGRDDAGEL	480
Qy	478	PAACVAVLESKTLTEKEVQDEFIAAOVTPRKLHRCGVGVVDSIPKPGTGLIRKELREIF-	536
Db	481	PAAVVAVLEHGTMEKEIVDAVASOYTTAKKLRGCVGVDEVBPGLTGKLDARKIREILI	540
Qy	537	-AORAPSKL 545 ,	
Db	541	KAKKGRSKL 550 :	

RESULT	5	
027668		
ID	027668	PRELIMINARY; PRT; 547 AA.
AC	027668;	
DT	01-NOV-1996 (Tremblrel. 01, Created)	
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)	
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)	
DE	PHOTINUS-LUCIFERIN 4-MONOOXYGENASE (Afp-HYDROLYSING) (EC 1.13.12.7).	
OS	Lampyris noctiluca.	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;	
OC	Elateriformia; Cantharoidea; Lampyridae; Lampyrinae.	
OX	NCBI_TaxID:41311;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=LIGHT ORGAN;	
RX	MEDLINE=96190714; Pubmed=8611152;	
RA	Sala-Newby G.B.; Thomson C.M.; Campbell A.K.;	
RT	"Sequence and biochemical similarities between the luciferases of the glow-worm Lampyris noctiluca and the firefly Photinus pyralis.";	
RL	Biochem. J. 313:761-767(1996).	
DR	EMBL; X89479; CAA61668.1; -.	
DR	HSSP; P08659; IICI.	
DR	InterPro; IPR000873; AMP-bind.	
DR	InterPro; IPR000215; Serpin.	
DR	Pfam; PF00501; AMP-binding. 1.	
DR	PROSITE; PS00455; AMP_BINDING. 1.	
DR	PROSITE; PS00284; SERPIN; UNKNOWN.1.	
QO	Monooxygenase; Oxidoreductase.	
QO	SEQUENCE 547 AA; 60365 MW; 8CB5653E0760D3EB CRC64;	

DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
KW Monooxygenase; Oxidoreductase.
SQ SEQUENCE 547 AA; 60365 MW; 8CB5653E0780D3EB CRC64

Query Match	54.6%	Score 1334	DB 5	Length 547
Best Local Similarity	53.5%	Pred. No. 4e-110		
Matches	293	Conservative 106	Mismatches 145	Indels 4
Gaps				3
QY	1	MEE-ENIRGGERPDIIVHGSAGOOLOYSLYTFAPSPPE--AIIIDATFNVISYAQFEENS	57	
DB	1	MDAKIMHIGPAPFYPFLEGTAGBOLHKMKRKRAOVPGTIIATFDAAEAVNITYSEFEENA	60	
QY	58	CLRAVSIEOYGLNENNVVGCSENNINFPNPLAALYLIGIPATSNDMYTDELTHENLI	117	
DB	61	CRLEATMKRYGIGLOHHIIVACSENSLOQFPMYOGALFIVGVASTNDINDINERELYSLSI	120	
QY	118	SKPTIMESSKKALPLILRYQOULSFKKKVVYIDSMTDINGVECVSTFYARVYDHTFDPLS	177	
DB	121	SOPTIVSCSKRALIKLIGVOKRLPIIOKLTIVIIDSDREDYMGKOSMYSFISHIPAGFENEYD	180	
QY	178	FPPKPFDPLEKIALIMSSSGTGTGPKGVVLSHRSILTRFVHSRDPYIGRTYDPTSILSL	237	
DB	181	YIPDSFDRETATALLIMSSSGTGLKRGVYLTHQNVCFRSHCRDPVFGMOIIPDAILITV	240	
QY	238	VPHHAFGNETTILSYFVVGKLYVMKLKKEFGALFLKTIONYKPIITVIVAPVWVFLAKSPL	297	
DB	241	IFPHGFGFMFTTLGYLTGCFRIVLWVRPEELFLNSLDIOYKIQSALLVPTLESFPAKSL	300	
QY	298	VNOYDLSLLEVAITGAPRGKDYAEAVAKRLPLGIIOGYGLTEFCAMVITPHNAVKTG	357	
DB	301	VKKYDLSNIHETASGAPRLAKEVEGAVARFKLPGIROGYGLTETTSAILIIRPEGDDKRG	360	
QY	358	SYGRPLPYIKAVLUNNATKALGPGRGKICQSEIMKGYNNPPEATIDTIDKQGLHS	417	
DB	361	ACGVVYVPEFSAKIYVDLDITGKITGVNORGLCYKGPIMKGYNNPEATISALIDKQGLHS	420	
QY	418	GDIGYVDEDDGNFFIVDRKLKELIKYGYOVAPEALENLLOHPSIADAGVYGVDERGGL	477	
DB	421	GDIAYYDKKGHFFIYDRKLSLIKYGQVPALELSILLOHFFIPDAGVAGIIPDPAGEL	480	
QY	478	PAAVCVLESGLKTEKEQODFIAQVTPYKHLRGVAVPDSIIPKPGTGLIKELREIFA	537	
DB	481	PAAVVLEBGMTEQEVMDYVAGOVYASKRLRGVKEVPEVPGKGLTGKIDGRKIREIL-	539	
QY	538	GRAPSKSL 545		
DB	540	MMGKSKSL 547		
RESULT	6			
ID	Q94696	PRELIMINARY:	PRT:	552 AA.
AC	Q94696:			
DT	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DE	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
LOC	LOC1FERASE.			
OS	Photuris pennsylvanica.			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
CC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;			
OC	Elateriformia; Cantharidae; Lampyridae; Photuris.			
OX	NCBI_TaxID=41716;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LANTERN;			
RA	Zenno S., Shiratsht S., Inouye S., Saigo K.;			
RT	"Cloning, nucleotide sequence and expression of two cDNAs encoding for			
RL	luciferase from Photuris firefly.";			
DR	Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; D25415; BAA05005.1; -.			
DR	HSSP; P08659; 1ICI.			
DR	InterPro: IPR000873; AMP-bind.			
DR	Pfam; PF00501; AMP-binding.1.			
DR	PROSITE; PS00455; AMP_BINDING.1.			
SO	SEQUENCE 552 AA; 61000 MW; 85C14ED52BD5366A CRC64;			

Query Match	54.0%	Score 1519	DB 5	Length 552
Best Local Similarity	52.8%	Pred. No. 5,9e-109		
Matches 287	Conservative 102	Mismatches 151	Indels 4	Gaps 3
QY	3	EEHHIRGEPRDIIVHGSAGOOLOSIFYEASPE--ATIIDHTNEVISAQIFERSCL	60	
Db	4	ENNIIIGPPPPYPLEEGSTAGEOIHRATITKAAVPGIATTDVHTELEVTYKEFLDYTCUL	63	
QY	61	AVSIEIYGLNENNYYGVCSENNINFEENPVLAALYIGIPVATSDMYDDELTHGHNISKP	120	
Db	64	AEAMKNYGLGHTHTISVCSENCVOEFMPYCALYIGVATAPNDIYNERELNYSISIQP	123	
QY	121	TIMFSSKAKLPLILKYOQNLSTFIKKVYVDSMYDINGVCVSTFPARTYDHFDELSPF	180	
Db	124	TVVFTSIRNSLQKILGVOSSLPIVIKITIMIDTKVDLGYOSMOSFKEHPANFNVAEPK	183	
QY	181	KPFDPLEKIALIMSSSGTGLPKGVLSHRSLTIRFVHSRDPYIGNRVPOTSILVPE	240	
Db	184	LSFD-LDRACIMNSSSGTGLPKGVPISHRNTTYRSHRDPVFGNQTIPDTTILCAVPE	242	
QY	241	HAHFGMTTLSYFVGLKVMKKEGALFLEKTIONYKTIPTITVAPVYVFLAKSPLYDQ	300	
Db	243	HAHFGFTMLGIIIGCFHVLMYRENEHFLQTDYKQOSALIVPTVLAFLAKNPLVDK	302	
QY	301	YDLSSTLTPATGAPLPGKVAFAVAKRLKLPBIIQGYGLTEFCCAVMTTPHAAVVTGSG	360	
Db	303	YDLSLHETIASGAPLSKISIEIAKRFPLPDIRQGYGLTEFTCAIVTAEGEFKPGAAG	362	
QY	361	RLPLPTIKAVLNLNATGKALGPERGEICQOSMIMKGYNNPEATIDTIDKGMVHSQDI	420	
Db	363	KVPEPSYLVKVDLNGTKKRIKPGNERGEICTGMIMKGYINNEARREIIDEGMVLHSDI	422	
QY	421	GYVDEGNEFIDRLKELIKYKGYOAPAELENLLQHPISADAGVYVDEFGQLPAA	480	
Db	423	GYFDEGHHYIVDRKLSTIKYGYVPAELFALLQHPFIEDAGVAGVDEVAADLPGA	482	
QY	481	CVLSESGKLTKEKQVDFIAQVPTFKHLRGVVVDSPKCPPTKILRIKELREIFAQRA	540	
Db	483	VVVLSEGSITKEKIDQIVAGOVTSKKILRGVEFEVPEKQFTGKIDTRIKETILTI-KA	541	
QY	541	PKSK 544		
Db	542	QKKG 545		
RESULT	7			
ID	Q94697	PRELIMINARY;	PRT;	552 AA.
AC	Q94697;			
DT	01-FEB-1997 (Tremblrel. 02, Created)			
DR	01-FEB-1997 (Tremblrel. 02, Last sequence update)			
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)			
DE	LOCIFERASE.			
GN	LOC.			
OS	Photuris pennsylvanica.			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;			
OC	Elateriformia; Cantharoidea; Lampyridae; Photuris.			
OX	NCBI_TaxID=41716;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LANTERN;			
RA	Zeno S., Shiratsht S., Inouye S., Saigo K.;			
RT	"Cloning, nucleotide sequence and expression of two cDNAs encoding for			
RL	luciferase from Photuris firefly."			
RL	Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; D25416; BAA05006.1; -.			
DR	HSSP; P08659; ILCI.			
DR	InterPro; IPR000873; AMP-bind.			
DR	Pfam; PF00501; AMP-binding.1.			
DR	PROSITE; PS00455; AMP_BINDING.1.			
SO	SEQUENCE 552 AA; 60970 MW; CAE619AE26561DE CRC64;			


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Query Match          53.9%; Score 1515; DB 5; Length 552;
Best Local Similarity 52.4%; Pred. No. 1.2e109;
Matches 285; Conservative 104; Mismatches 151; Indels 4; Gaps 3

OY 3 EENINGERPRDVIHPGSGAQQLOYSLKFAFSE--AIIADHTNEVISYAOIFETSCRL 60
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 4 ENNIIIGPPPPVPLEEGVAGAEQDLHRAISRVAAPGTLAVTDVHTLELVYKKEFLDVTCK 63

OY 61 AVSIQGYGLNENNVYGVSENNINFPNVLALYLGIPATVNDMTTDOELGHLINISRP 120
   : : :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 64 AEAAMNNYGLGLOHTISYVSENCVQEFMPICALYVGVATAPNDINDIRELNLSISQ 123

OY 121 TIMFSSKALPLILRVQONLSFIRKVVVDSMYDINGVCSVFARVYDHTFPLSTFP 180
   | : | : |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 124 TVVFTSRNSLQKIIIGVQSRPLPIKKIIIIIDGKKDVLGYQSMQSPKHEHPANFNVSAPFR 183

OY 181 KQDFPLEKIALIMSSGTTGPKGVVLSHRSLTIRFVHSRDPYIGTRVYQTSISLVP 240
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 184 LSFID-LDRVACIMNSSGSGTGLPKGVPSIRNITYRFSHCRDVFCNQIIPDTIILCAVP 242

OY 241 HHAFCMEPTLSFVGVGLKVMMLKREGALFLEKTIONYKPTIVVAPRVVFLAKSPLYQ 300
   ||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 243 HHAFTFTNLGLLIGCFHVLVYLRNENHLEFQTLQDYQKQSLALVFTVLAFIAPKPLVVK 302

OY 301 YDLSLLEVTATGGAALGKDVAAEVAKRLKLPILIOGYSGLTEFCAAVMTIRHNAVKTGSTG 360
   ||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 303 YDLSMLHEIASGAPARLSKREISIAAKRFLPGIRQGYGLTEITCALVIAEGEFKLGAVG 362

OY 361 RPLPIITAKVLDNATGKALGPERGEICQOSEIMKGYNNPEATIDTIDKQGLHSGDI 420
   : : :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 363 KVPPEISLKVLDLNTGKKIGPNEREEICKPGIMKGYINNEAPARELLIDEGWHISGDI 422

OY 421 GYVDDGNGFFIYDRKLKELIKYGVAPAELENLLLOHPSIDAGVGYVDEFGOLPPAA 480
   ||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 423 GFDEDDGHVYIVDRKLSLTKYGVVAPRAELALLLOHFIEDAGVAGVPDEVAQDLPPGA 482

OY 481 CYLEESGKTLTEKEVQDFTAAOVTPPKILRGVVFVDSIPKCGTGLKRLKELREIFAQRA 540
   |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 483 VVLEEGKSITPEKETIDYVAGQVTSKKLRGGEVEFVKEVPKGTGKIDIRKIKEILI-RA 541

OY 541 PKSK 544
   |  |
Db 542 OKKG 545

RESULT 8
O26076 PRELIMINARY: PRT: 548 AA.
AC O26076:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DR 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE LUCIFERASE.
DOS Pyrococcus abyssi.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Elateriformia; Cantharidae; Lampyridae; Pyrococella.
OX NCBI_TaxID=33963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96061635; PubMed=7480137;
RA Ohmura Y., Ohba N., Ton H., Tsuji F.;
RT "Cloning, expression and sequence analysis of cDNA for the luciferases
RT from the Japanese fireflies, Pyrococella abyssi and Hotaria parvula.";
RL Photochem. Photobiol. 62:309-313(1995).
DR EMBL: L39928; AAC37254.1; -.
DR HSSP: P08659; ILCI.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR000213; Serpin.
DR Pfam: PF00501; AMP-binding; 1.
DR PROSITE: PS00455; AMP_BINDING; 1.

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DR	PROSITE: PS00284; SERPIN; UNKNOWN_1.	
SEQ	SEQUENCE 548 AA; 60956 MM; CD37F63E982A9401 CAC64;	
	Query Match	53.8%; Score 1511.5; DB: 5; Length 548;
	Best Local Similarity	52.9%; Pred. No. 2,2e-108;
	Matches 289; Conservatively 103; Mismatches 151; Indels 3; Gaps	
OY	2 EENRTRHGERPRDIYHPSAGQOLYSLTKFASFE--AIDAHNEVSYAOIFETSCR 59	
DB	4 DSKHIMHGHRHSILWEDGAGLOLHKAMKRYAOVGGTILFTDAHAEVNITYSEYFEMSCR 63	
OY	60 LAVSYEYGLNENNVGVGSENNINPFNVLAALYIGIVPATSNMPTGTGLGHNISK 119	
DB	64 LAETMKRIGLGIQHIIHVAVSETSLOPFMYCALITGVAAPFDNDYNERELNSLFIQO 123	
OY	120 PTIMSSKKALPDLIRVOONLSFIKKVVYIDSMYDINGECVSTFVARYTDHFDPLSFT 179	
DB	124 PTLVSCSKALOKLILGVOKKLPVIOKIVILDSREDYMGQMSYFSLHLPAGFNEYDYI 183	
OY	180 PRDEPRLKIALIMSSSGTTGLPKGVVLSHRSILTRFVHSRDPYIGTRVPOTSLSLVP 239	
DB	184 PDSFRETATALIMSSSGSTGLPKGVDTLHMVVCVRFSCRPVFQNOIIPDTALITVIP 243	
OY	240 FHHARGMFTTSLFYVGLKVVMLKKFEGALFTKTONYKILPIITVAPRVMLFASPLVD 299	
DB	244 FHHVQMFPTLGLYLCGFRIYLMREERELFRLSLDDYIQSALLPLTFSFASSTLVD 303	
OY	300 QYDLSLFTVANGAPRLKRDVAEAVAKRLKGLIIGYGLTETCCAVMTPHNAVVTGST 359	
DB	304 KIDLSTLHETIASGAPRLAEVGEAAVKRRKRLGIRGYLTLETTSAILTTPEDDKRGAC 363	
OY	360 GRPLPIKAKVLDNATGKALGPGERGEICFQSEMIIMKGYNNPEATIDTIDKDWLHSD 419	
DB	364 GKVPFEFTAKIVYDLDTGKTLGVNQBELCVKPMIKRGVNNPEATNALIDKDWLHSD 423	
OY	420 IGYVDEGNGFTVYDRLKELIKYGVAVAELENNLHPSHSTADGVTPREFGGLDA 479	
DB	424 IAYVDDGHEFTVYDRLKSLIKYGVAPRAELISILHPPFDGVAAPIPDDAELPA 483	
OY	480 ACVVLSEGTLEKEVQDFEIAQVPTFKHLRGVAVFSDIPKPGPTKLIRKLEIREIFAOR 539	
DB	484 AAVVLEEGKMMTEQEVMDVYAGVYATSKRLRGVAKYVDEVPGKLTICKIDSKRIRELTM- 542	
OY	540 APKSKL 545	
DB	543 GOKSKL 548	
RESULT 9		
O9GPF9	PRELIMINARY; PRT; 548 AA.	
AC	O9GPF9;	
DT	01-MAR-2001 (TREMBLREL. 16, Created)	
DT	01-MAR-2001 (TREMBLREL. 16, Last sequence update)	
DT	01-DEC-2001 (TREMBLREL. 19, Last annotation update)	
DE	LUCIFERASE.	
OS	Pyrococella rufa.	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;	
OC	Elateriformia; Cantharoidea; Lampyridae; Pyrococella.	
OX	NCBI_TaxID=71223;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=LIGHT ORGAN;	
RA	Lee K.S., Park H.-J., Bae J.S., Lee K.S., Shon H.D., Jin B.R.;	
RT	"Molecular Cloning and Expression of cDNA encoding luciferase from the	
RT	firefly, <i>Pyrococella rufa</i> ."	
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AF328553; AAG45439.1; -	
DR	HSP: P08659; ILCI.	
DR	InterPro: IPR000215; Serpin.	
DR	PROSITE: PS00284; SERPIN; UNKNOWN_1.	

DR InterPro: IPR0000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PROSITE: PS00455; AMP BINDING;
SQ SEQUENCE 548 AA; 60495 MW; 62C8953BDFBC423 CRC64;

Query Match	52.7%;	Score 1483;	DB 5;	Length 548;
Best Local Similarity	52.0%;	Pred. No. 3.6e-106;		
Matches 284;	Conservative 107;	Mismatches 151;	Indels 4;	Gaps 3

Oy		2	EENINRHEREDRPDYVHGSAAQOOLYSGLRKSPPE-AIIDATHNEVSYAOJLEFSCR	60
Dd		5	KENNYYGRLPFYITEEGSAGIOUHKIMHOYAKALGAIAFSNALTGVDSIQEFPDITCRL	64
Oy		61	AVSIEOYLGNENNIVGYGCSENNINFNPVLAALYIGIPATSDMYTDGELTGLNLISKP	120
Dd		65	AAMKNFCMKPDEHIALCSENCEBFFIPVLADGIYGAVAAPTEIYTLRELNLNSIIAQI	124
Oy		121	TTFSSSKALFLILRVQONLSFIKKVVYIDSMHDINGECVSIFVARYTDTHTDPLSFTR	180
Dd		125	TIVSSSRGKLPRVLEVOKRTVCIKKIYILDISKVNFGGHDDMETEFIKKHVELGFQPSFEV	184
Oy		181	KDF-DPLEKIALINSSGGTTGLPKGVVLSHRSLIRFVHSRDPYGRTRVPOTSITLVP	239
Dd		185	IDVKRRKOVALLNMSGSGTGLPKGVRIITHEGAATRFSHKDDPLYGMQVSPGTALLTVP	244
Oy		240	FHAHAFGMTFTLSFYVVGILKVMMLKEFGALFKTIQNYKAIPTIIVAPPVAFIASKPLVD	299
Dd		245	FHHGGMTTTTGITGYACGVRVWMLKPDDELFRITLDQYKCTSVILVPTLLAILNKSELID	304
Oy		300	QYDSSLTEVATGAPLGKDVAEAVARLKLPGLIIQGYGLTECCAVMTTPHNAVKTGST	359
Dd		305	KFDLSNLTEIASGAPLAKKEGEVAARFNLPVGRQGYGLTEETSAFIIIPGEDDKPGAS	364
Oy		360	GRLPYIRAKULDMNATGAKALGPGRGRTICQOSEIMMGYNPNPATDITDIKOGMLHSGD	419
Dd		365	GKVPAFLVAKVIDDITDKTKLVNRGSELCVAKGPSLMILGYSNNPARETRIDECSGHLTGD	424
Oy		420	IGYDEDENFEITYDRLEKELIKYKGQYAAPALEMULLLOHPISIADAGVTGPDEFGOLPA	479
Dd		425	IGYDEDDHEFTIVDRKLSLIKRYQYPRALESVILLQHNIPIFDAGVAGVPPDDAGLPG	484
Oy		480	ACVVEESGKTLEKEVODIFAQVTPRKHLRGVVEVDSIPKGPBGKLIKKELREIFPAQR	539
Dd		485	AVVMEKCKTTEKEIYDVYNSQVNVNHKRILGRGVFDEVBPGLTKRIDAKVIREIL--K	542
Oy		540	APKSTL 545	
Dd		543	KPOAKM 548	
RESULT		12		
Q27348				
ID	Q27348	PRELIMINARY;	PRT; 548 AA.	
AC	Q27348:			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	LUCIFERASE.			
OS	Luciola lateralis (Firefly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;			
OC	Elateriformia; Cantharoidae; Lampyridae; Luciola.			
OX	NCL_TaxID=7052;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MUU; TISSUE=ABDOMEN;			
RA	Cho K.H., Choi Y., Boo K.;			
RL	Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=MUU; TISSUE=ABDOMEN;			
RA	Cho K., Choi Y., Boo K.;			

RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases
 DR EMBL: U49182; AA81472.1; -
 DR EMBL: Z4981; CAA90072.1; -
 DR HSSP: P08659; 1ICI.
 DR InterPro: IPR000873; AMP-bind.
 DR Pfam: PF00501; AMP-binding; 1.
 DR PROSITE: PS00455; AMP_BINDING; 1.
 SQ SEQUENCE 548 AA: 60062 MW: D237F6EC97CA3BBD CRC64;

Query Match	51.8%;	Score 1457.5;	DB 5;	Length 548;
Best Local Similarity	51.8%;	Pred. No. 3.3e-104;		
Matches 282;	Conservative 101;	Mismatches 158;	Indels 3;	Gaps 2

Oy	3	EEERHGRPRPDIVHVGAGQOLVSYLKFKA\$PDE--AIDAHTNEV\$SYAOIFET\$SURLA	61
Oy	7	DENYIVGKPPRIPIIEBSGAGQOLKRYMDRIKALCALAFNLTGCVDTYVAYEYLEK\$SCCLG	66
Oy	62	VSIEOYGLNENNVGVCS\$ENNIINFENPVLALYLGIVAT\$NDMYTGTGELTGLHNL\$KPT	121
Oy	67	EALKMYGLVNDGRIALCE\$NEEEFIPYLAGLFGVGVAPN\$EYTLRELVLH\$GLSKPT	126
Oy	122	IMF\$SKKALPILRVQNL\$FIRKVVVID\$MYDINGVECV\$ESTVARYT\$DHTFDP\$LSFTPK	181
Oy	127	IVF\$SKKGLDKVITVQ\$KTVNAIKTIVILDSKVDRYGV\$Q\$MDNFIKKNT\$PGFK\$SSEKTV	186
Oy	162	DEDPLEKIALIM\$SSGTTGLPKGVYLSHR\$LTIRFVHSRDPY\$GTRV\$PQTSIL\$VPEH	241
Oy	167	EYNRKEOYVALLMNS\$G\$TGLPKGVQ\$LT\$HENA\$VTRF\$SHARDPY\$GNQV\$SGTALITVPEH	246
Oy	242	HAFGEFTLSYF\$VVGGLKRVMLK\$FEGAL\$FTKIONYKIP\$TVAP\$P\$WFLAK\$SPLYDOX	301
Oy	247	HGFGEFTLYGLT\$GFCFRV\$MLTK\$FDEETFL\$TLDYD\$C\$SYILPVL\$FALLN\$SELDKY	306
Oy	302	DLS\$TEVAT\$GAPL\$GKGVAA\$VAA\$KRLKLP\$IIIOGYGLT\$ETCC\$AMITP\$HNAV\$T\$G\$TGR	361
Oy	307	DLSNLYELIASG\$APL\$SKRIG\$EAVAR\$RFLP\$BVRQYGLT\$ET\$S\$AITTP\$EDDK\$P\$ASGK	366
Oy	362	PLPYIKARVLDNAT\$GKAL\$G\$E\$RGEI\$CFQ\$SEM\$IKGY\$N\$N\$EATIT\$DITDKGWL\$HSDIG	421
Oy	367	VYPLEFKAVIDLP\$TKTGL\$P\$RRR\$E\$C\$V\$G\$M\$LAK\$G\$VDN\$EAT\$REIL\$IDEGW\$LHT\$DIG	426
Oy	422	YYDEG\$NFYIDRLKELIKY\$GYQVAP\$ELENLLQ\$H\$P\$TAD\$AGV\$P\$DEFGQ\$LPAC	481
Oy	427	YYDEK\$H\$F\$YIDRLKSLIKY\$GYQVAP\$E\$LSYLLQ\$H\$N\$T\$F\$D\$AC\$V\$P\$P\$D\$IA\$E\$LG\$AV	486
Oy	482	VYLE\$GKTLTE\$E\$VOD\$F\$IAA\$V\$OT\$P\$TKHL\$RG\$V\$V\$D\$S\$IPK\$PT\$K\$LRKEL\$REI\$FAOR\$AP	541
Oy	487	VYLE\$GK\$MTE\$E\$VAD\$Y\$VAGOV\$SNAKRL\$RG\$V\$R\$E\$V\$D\$E\$P\$K\$GLIC\$IDG\$KAI\$REIL--KRP	544
Oy	542	K\$KL 545	
Oy	545	VAKM 548	
RESULT	13		
ID	027757	PRELIMINARY; PRT; 545 AA.	
AC	027757; 002653;		
DT	01-NOV-1996 (Tremblrel. 01, Created)		
DT	01-JUL-1997 (Tremblrel. 04, Last sequence update)		
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)		
DE	LUCIFERIN 4-MONOOXYGENASE (EC 1.13.12.7) (LUCIFERASE).		
OS	Photuris pennsylvanica.		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;		
OC	Elateriformia; Cantharoidea; Lampyridae; Photuris.		
OX	NCBI_TaxID=41716;		
RA	SEQUENCE FROM N.A.		
RC	TISSUE=LANTERN;		
RA	MEDLINE=97307756; PubMed=9165098;		
RA	Ye L., Buck L.M., Schaeffer H.J., Leach F.R.;		

RT	Cloning and sequencing of a cDNA for firefly luciferase from Photinus		
RT	pennsylvanicus. ⁷		
RL	Biochim. Biophys. Acta	1339:39-52(1997).	
CC	-1-	FUNCTION: PRODUCES GREEN LIGHT WITH A WAVELENGTH OF 562 NM (BY SIMILARITY)	
CC	-1-	CATALYTIC ACTIVITY: PHOTINUS LUCIFERIN + O(2) + ATP -> OXIDIZED PHOTINUS LUCIFERIN + CO(2) + H(2)O + AMP + DIPHOSPHATE + LIGHT.	
CC	-1-	COFACTOR: REQUIRES A MAGNESIUM ION (BY SIMILARITY).	
CC	-1-	SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).	
CC	-1-	SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.	
DR	HESBL; U31240; AAB60897.1;	-	
DR	HESBP; P08659; ILCI.		
DR	InterPro: IPR000873; AMP-bind.		
DR	Pfam: PF00501; AMP-binding; 1.		
DR	PROSITE: PS00455; AMP-BINDING; UNKNOWN 1.		
KW	Oxidoreductase; Monooxygenase; Photoprotein; Luminescent; Magnesium; Peroxisome.		
FT	SITE	543	545 MICROBODY TARGETING SIGNAL (POTENTIAL).
SO	SEQUENCE	545 AA;	60649 NM; F0FE4EB28047C26E CRR64;

Query Match	51.7%	Score 1454	DB 5	Length 545
Best Local Similarity	50.1%	Pred. No. 6.2e-104		
Matches 274	Conservative 111	Mismatches 158	Indels 4	Gaps 2

QY	1	MEENIRGEGPRDIIHVHSGSGOOLYOSIKFAFEPF--AIIDHTEIVSYAQIPETSC	58
Db	1	MEDKNILILGPEFPHRLADGTAGEOMFALSKYADISCIALTNAHTENWLYEEFLKSC	60
QY	59	RLAVSIEOYGLNENNVYGVCSENNINFENPYLAALYIGIPVATSDMYTGDGLGHNIS	118
Db	61	RLASFEEKYQKJNDJTIAACSENGLOFPLRLIASLYGIIAAPVSDKYIERELIHSIGIV	120
QY	119	KPTIMFSSKRLPLILRVQOOLSTIKKVVYIDSMTDINGEBCVSTFARTTDHTEPLSF	178
Db	121	KPRILFCSKNTFOKVLNWKSLKLYVETIIILDINEDLGGYOCLNNFTSONSDINLDVKPF	180
QY	179	TPKDFDPLEKLTALIMSSSGTGLRGVLSHRSLTIEFHSRDPYGTGRVPOSTISLV	238
Db	181	KPNSFNBDQVALMFESSSGTTGVSKGYMLTHKNIVAFHSCKDPTFENALINPTAILITVI	240
QY	239	PFHHAFGMFTLLSYFVYVGLKRVMLKKEGALFLEKTIONKXIPITIVAPRVWELAKSPV	298
Db	241	PFHHGFGMTTLTGFEYCGFVRVYALNHTPEEKLFIQSLDQYVESLILVPTIMAFPPKSALV	300
QY	299	DQYOLSLTEVATGAPRLGKDVAEVAVKRLKPEIIOGTGLTETCCAVMITPHNAKVTGS	358
Db	301	EKYDLSHLEKIASGAPRLSEIGEMVKKRKLNFVRQGYLGTETTSVAILITPDTVBPVGS	360
QY	359	TGRPLPYTKAVALNNGAKLNGPEERREIOFQSGMINKGYNNPEARTIDIDKDGWHLHG	418
Db	361	TGKLTVPFPAKVAVNDPTTGKILIGPRETELFEFKGDMIKSYNNNEAKRALINKDGWRJSG	420
QY	419	DIGYDEDEGNFIYDRLEKILIKYGYOVAPAELENLILHPSIADAGVGTVPDEFGOLP	478
Db	421	DIAYYDNDGHHYIYDRILKSLIKYGYOVARAEIEGILLOPIRYIYDAGVSTIPDEACELP	480
QY	479	AACVYLESKGTLEKEVODFPIAAOVTPYTKHLRGGVFVDSIPKGPYTKLRLEIRELFAQ	538
Db	481	AAGVYVOTGKYLINQOIVONEFVSSQVSTPAKMLRGVVKFLDEIPKSGSTGIDRKVLRQMFEX	540
QY	539	RAPRSKUL 545	
Db	541	H--RSKL 545	

RESULT	14	
Q27321		
ID	Q27321	PRELIMINARY;
AC	Q27321;	PRT; 548 AA.
DT	01-NOV-1996	(TREMBlE1. 01, Created)
DT	01-NOV-1996	(TREMBlE1. 01, Last Sequence update)

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DF 01-JUN-2001 (TremblereL. 17, Last annotation update)
DE LUCIFERASE.
OS Luciola lateralis (Firefly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Elateriforma; Cantharoidea; Lampyridae; Luciola.
OX NCBI_TaxId=7052;
RN [1]
RP SEQUENCE FROM N.A.
RA Cho K., Choi Y., Boo K.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Cho K.H., Choi Y., Boo K.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-MUTJ; TISSUE=ABDOMEN;
RC Cho K., Choi Y., Boo K.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z69619; CA93444.1; -.
DR EMBL; U49181; AAA91471.1; -.
DR EMBL; U51019; AAB00229.1; -.
DR HSSP; P08659; 1LCI.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP-BINDING; 1.
SQ SEQUENCE 548 AA; 60048 MW; E26CEC26F423E5EB CRC64;

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Query Match	51.7%;	Score 1453.5;	DB 5;	Length 548;
Best Local Similarity	51.7%;	Pred. No. 6.8e-104;		
Matches 281;	Conservative 102;	Mismatches 158;	Indels 3;	Gaps 2;

[illegible]

DB 545 VAKM 548

RESULT 15

09VCC6 PRELIMINARY; PRT; 544 AA.

ID 09VCC6; 09VCC6;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE CG6178 PROTEIN (GMO5240P).

OS CG6178.

GN *Drosophila melanogaster* (Fruit fly).

OC Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_taxid=7227;

ON [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,

RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borokova D., Botchan M.R., Bouck H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke K., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Dou P.L.E., Donnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fostler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ilegvam C.,

RA Jaisl M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of *Drosophila melanogaster*.";

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

RA Nuno J., Pacled J., Paragas V., Park S., Phouanavong S., Wan K.,

RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AE003746; AAF56245.1; -

DR EMBL: AY060906; AAL8454.1; -

DR HSSP: P08659; 11CI

DR FlyBase: FBgn0039156; CG6178.

DR InterPro: IPR000873; AMP-bind.

DR Pfam: PF00501; AMP-binding; 1.

DR PROSITE: PS00455; AMP_BINDING; 1.

SQ SEQUENCE 544 AA; 59938 MW; E2B88DADCC988F3C CRC64;

Query Match 36.6%; Score 1030; DB 5; Length 544;

Best Local Similarity 41.38; Pred. No. 3.7e-71;

Matches 230; Conservative 102; Mismatches 183; Indels 42; Gaps 10;

12 PRODIVP-----SAGQOLYQSLYKFAFPPE--AIIIDANTNEVISYAOIFETSC 58

17 PGNIVYGGPPTERQADQSRSLGQYI---LQKYSFGGRIVLVADVNEVESASPMHMSIV 63

59 RLAVSIQYGLNENNVVGVCSENNINFPNPLAALYLGIPVANSNDYTDGELTGHNLIS 118

64 RLAVIQLKGLKQNDVYGLSSNSVNFALMFAAGATVAPLVNYSREVDHAINLS 123

119 KPTIMSSKRALPILVQOQLSFIKRVVID-----SNYDNGVECVSTFARTDH 171

124 KPRIIFASKITIDRVAAVASKNKFVKGIILSGTSKFKFNIDYDKEI-----MEDE 174

172 TFDPL-SFTPKDPLKRIKALINSSGTTGLPKGVLSLTFRFVHSRDPYGTPTVP 230

175 KFTQDPPTSPANKDDEVSILVSSGTTGLPKGVLTOMNLATDSQIOP-----TVIP 230

231 --QTSILVLPFHAFGMFTTSLYFVGLKVMYMKKEGALFETKTONYKIPITVAPV 288

231 MEEYTLTLVIFWFAFGCLTLITACVGARLVYLPKFEKELFLSAIKRYMAFVYVPL 290

289 MVLAKSPVDQYVLSLTVATGAPLGVKVAVAVKRLKLPISIDGYGTETCCAVMI 348

291 MVLAKHPYDKYDLSLMLVLCGAAPLSRETQIKERIGVPIRGYGLSESTLSLV 350

349 TPNAVKTGSTRPLPYIKAKVLDNATGKALGPGESEICFQSEIMKGYNNPEATIDT 408

351 ONDEFCKRPGSVGLKVGIAKVIDPDGTGLGANERELCKGKGIMKGYIGDKST-QT 409

409 IDKQGLHSGDIGYDEDEGNFIYDRKELIKYGYOAPAELENLLQHPSTADAGYTG 468

410 AIKGMWLTGDIYDDDFEYFIDRIKELIKYGYOVPPAEIALLTNDKIXDAVIG 469

469 VPDEFGOLPAACVVLBSGKTLTEKEYODFIAQVTPFKHLRGVGVVDSIPKPGTKLI 528

470 KPDEAGGLPLAFVVKQANNVLTENEYIOFVNDNAPKRLRGVIVDEIIPKPSGKIL 529

529 RKELEIFQAPRPSKL 545

530 RLIREMLKKQ--KSKL 544

Search completed: September 4, 2002, 15:07:47

Job time: 246 sec

